

Fig.1.

*Pst*I

CAGGTGCAGCTGCAGGAGTCAGGGGGAGGATTGGTGCAGGCTGGGGGCTCTCTGAGACTC
 Q V Q L Q E S G G G L V Q A G G S L R L

TCCTGTGCAGCCTCGGGACGCGCCACCAGTGGTCATGGTCACTATGGTATGGGCTGGTTC
 S C A A S G R A T S G H G H Y G M G W F

CGCCAGGTTCCAGGGAAGGAGCGTGAGTTTGTGCGCAGCTATTAGGTGGAGTGGTAAAGAG
 R Q V P G K E R E F V A A I R W S G K E

ACATGGTATAAAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGATAACGCCAAGACT
 T W Y K D S V K G R F T I S R D N A K T

ACGGTTTATCTGCAAATGAACAGCCTGAAACCTGAAGATACGGCCGTTTATTATTGTGCC
 T V Y L Q M N S L K P E D T A V Y Y C A

GCTCGACCGGTCCGCGTGGATGATATTTCCCTGCCGGTTGGGTTTGACTACTGGGGCCAG
 A R P V R V D D I S L P V G F D Y W G Q

GGGACCCAGGTCACCGTCTCCTCAGAACAAAACTCATCTCAGAAGAGGATCTGAATTAA
 G T Q V T V S S E Q K L I S E E D L N

TAAGGGCTAAGCTCGAATTC
 EcoRI

Fig.2A.

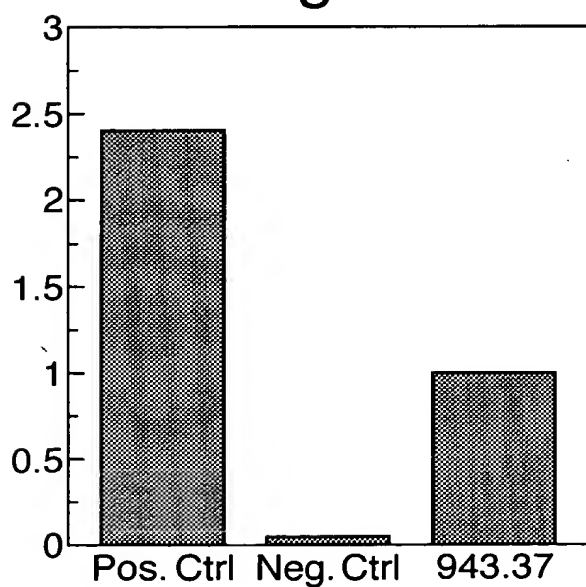


Fig.2B.

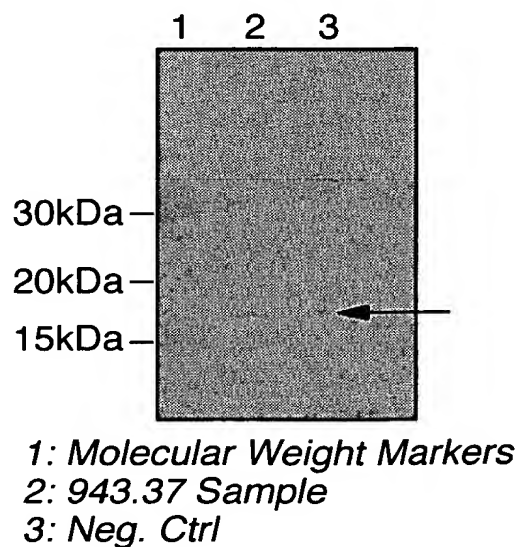


Fig.3A.

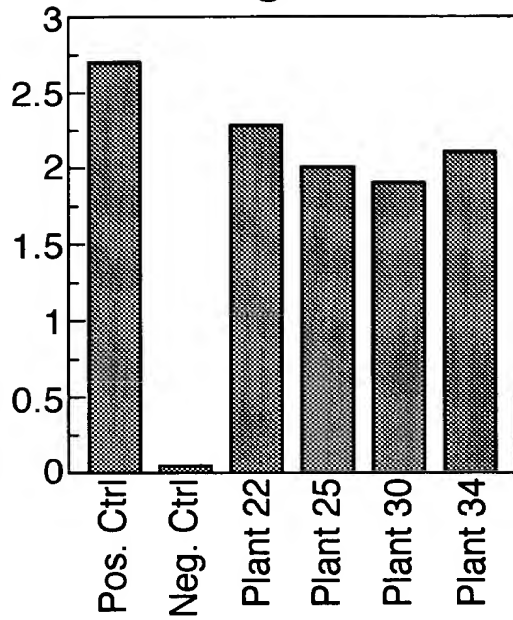


Fig.3B.

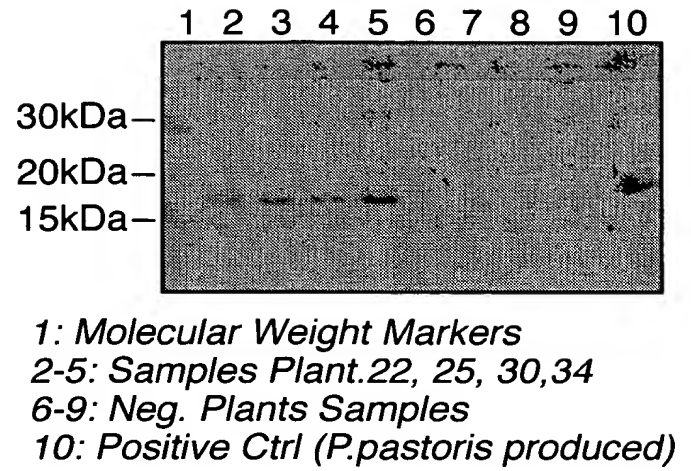
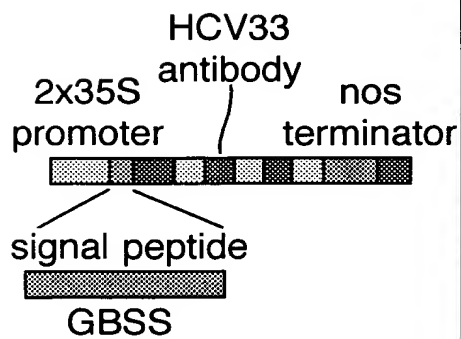


Fig.4.



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Fig.5.

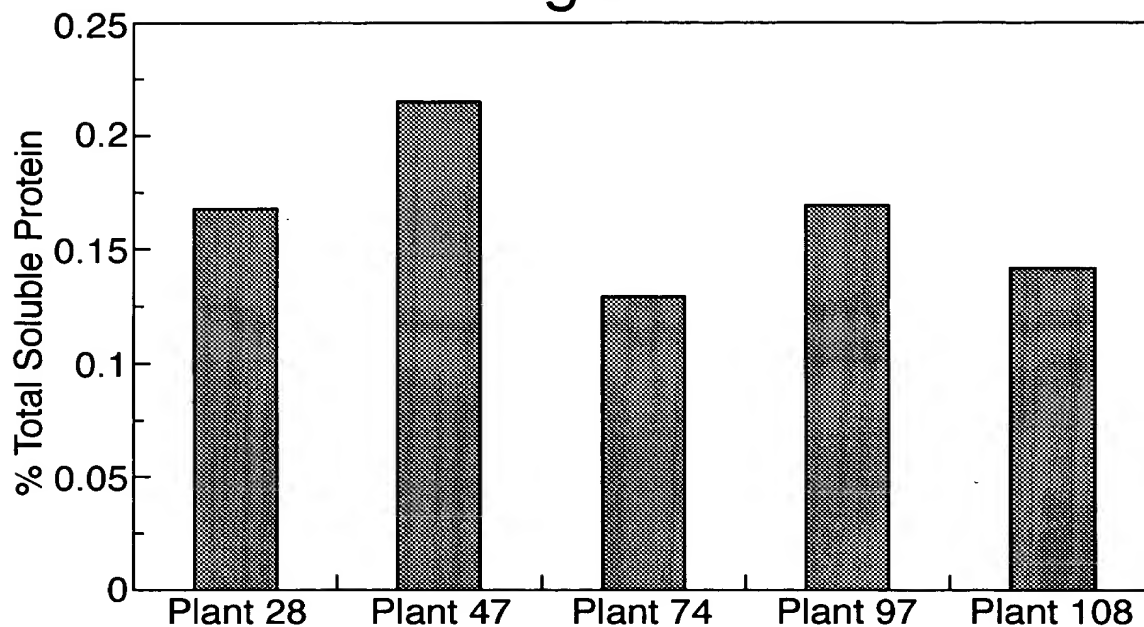


Fig.6.

*Pst*I

CAGGTGCAGCTGCAGCAGTCAGGGGGAGGCTTGGTGCAGGCTGGGGGGTCTCTGAGACTC
 Q V Q L Q Q S G G G L V Q A G G S L R L
 TCCTGTGTAGCTTCTGAAAGCAGCTTCAGCAACAATCACATGGGCTGGTACCGCCGGGCT
 S C V A S E S S F S N N H M G W Y R R A
 CCAGGGAACCAGCGCGAGCTGGTCGCAACTATTAGTCCTGGTGGTAGCACACACTATGTA
 P G N Q R E L V A T I S P G G S T H Y V
 GACTCCGTGAAGGGCCGATTACCATCTCCCGAGACAACGCCAAGAACACAGTGTATCTA
 D S V K G R F T I S R D N A K N T V Y L
 CAAATGGACAGCCTGAAACCAGAGGACACGGCCGTCTATTACTGTGCTGCCAAGGGGAGG
 Q M D S L K P E D T A V Y Y C A A K G R

*Pst*I

GGGCTGCAGGCTATGCAGTACTGGGGCCAGGGGACCCTGGTCACCGTCTCCTCAGCGCAC
 G L Q A M Q Y W G Q G T L V T V S S A H
 CACAGCGAAGACCCAGCTCCGCGGCCGCCCATCACCATCACCATCACGGGGCCGCAGAA
 H S E D P S S A A A H H H H H H G A A E
 CAAAACTCATCTCAGAAGAGGATCTGAATGGGGCCGCATAGTAACAATTG
 Q K L I S E E D L N G A A *Mun*I

Fig.7.

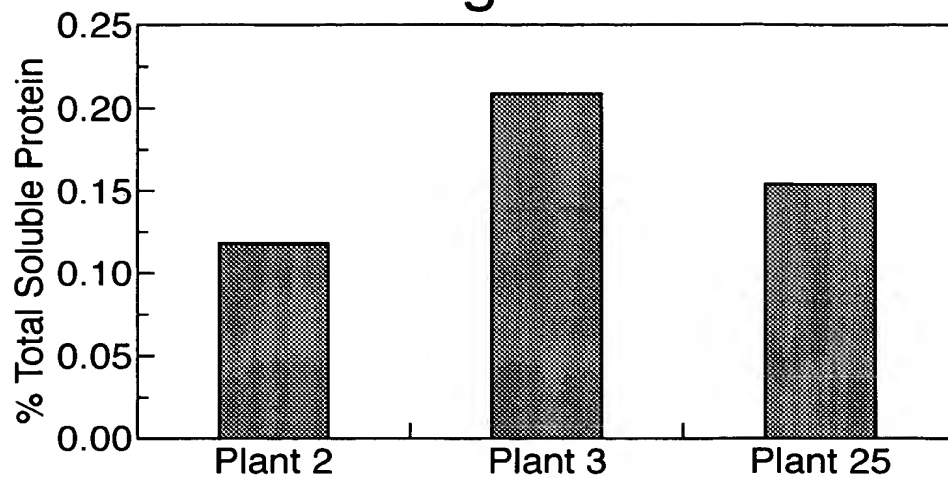


Fig.8.

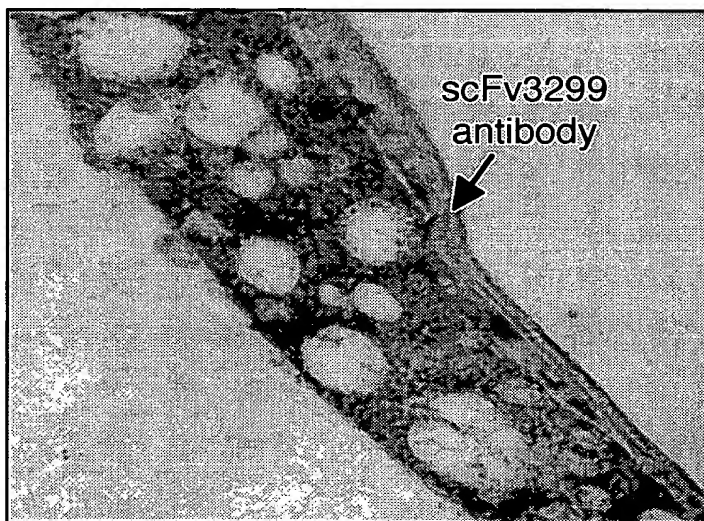
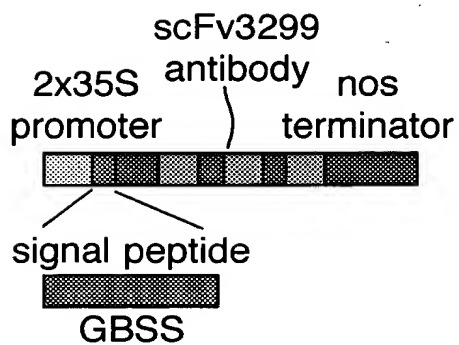


Fig.9.

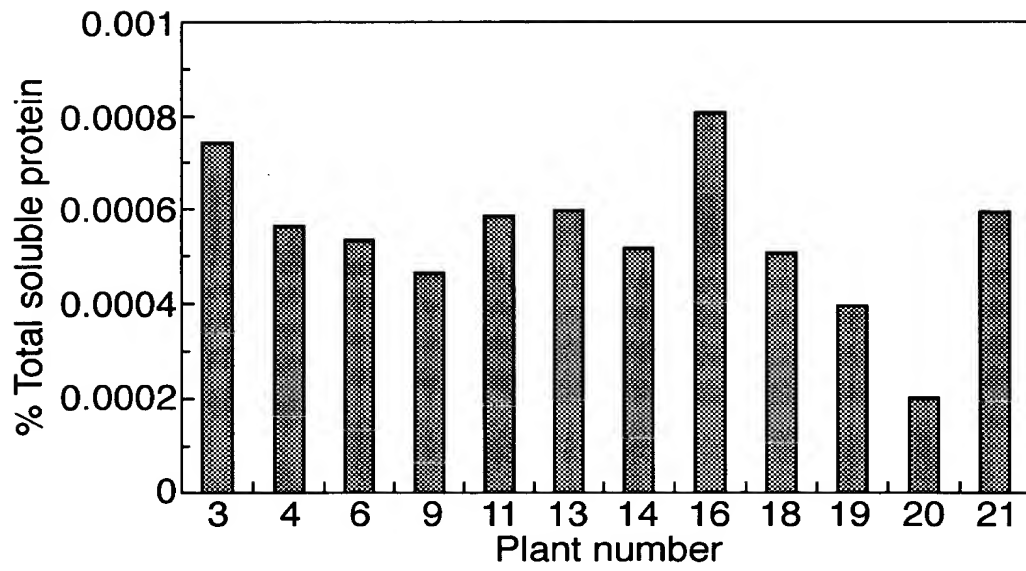


Fig.10A.

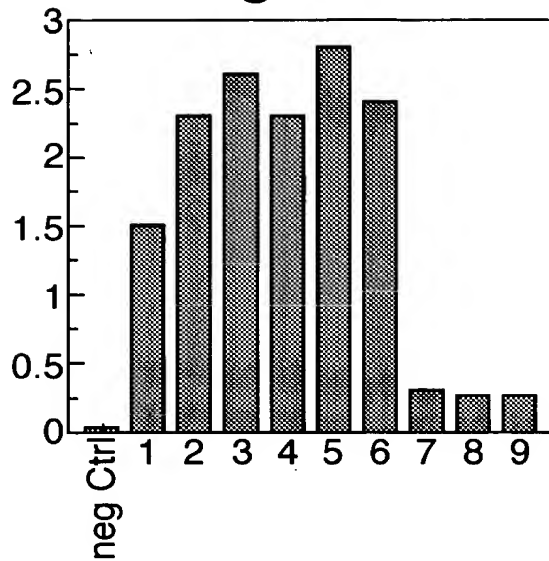
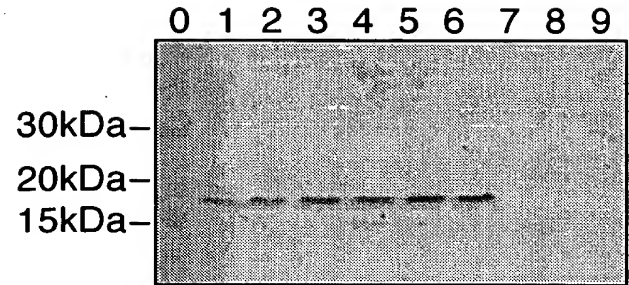
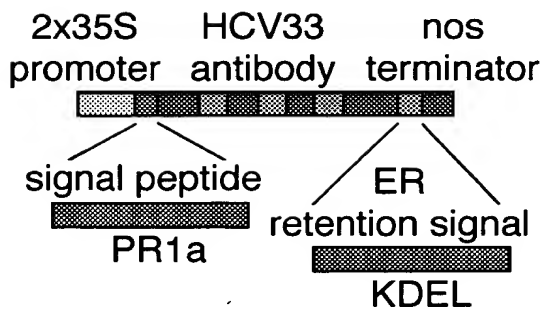


Fig.10B.



0: Molecular Weight Markers
 1-6: pPV.8-PR1a-HCV33-
 myc-SKDEL plants
 7-9: pPV.8-GBSS-HCV33-
 myc-SKDEL plants

Fig.11.



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Fig.12.

*Pst*I
CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCCTGGTGCAGGCTGGGGGGTCTCTGAGACTC
Q V Q L Q E S G G G L V Q A G G S L R L
TCCTGTGTAGCCTCTGGAACACCTTCAGTATCATAGCTATGGCCTGGTACCGCCAGGCT
S C V A S G N T F S I I A M A W Y R Q A
CCAGGGAAGCAGCGCGAGGTGGTTCGCAAGTATTAATAGTATTGGCAGCACAAATTATGCA
P G K Q R E V V A S I N S I G S T N Y A
GACTCCGTGAAGGGGCGATTACCATCTCCAGAGACAACGCCAAGAACACAGTGTATCTG
D S V K G R F T I S R D N A K N T V Y L
CAAATGAGCAGCCTGAAACCTGAGGACACGGCCGTCTATTACTGTGCTGCCGGTAATTTG
Q M S S L K P E D T A V Y Y C A A G N L
CTGGTTAAGAGGCCTTACTGGGGCCAGGGGACCCTGGTCACCGTCTCCTCAGAACCCAAG
L V K R P Y W G Q G T L V T V S S E P K
ACACCAAACCACAACCAGCGGCCGCCCATCACCATCACCATCACGGGGCCGCAGAACAA
T P K P Q P A A A H H H H H H G A A E Q
AAACTCATCTCAGAAGAGGATCTGAATGGGGCCGCATAGTAACCAATTG
K L I S E E D L N G A A *Mun*I

Fig.13.

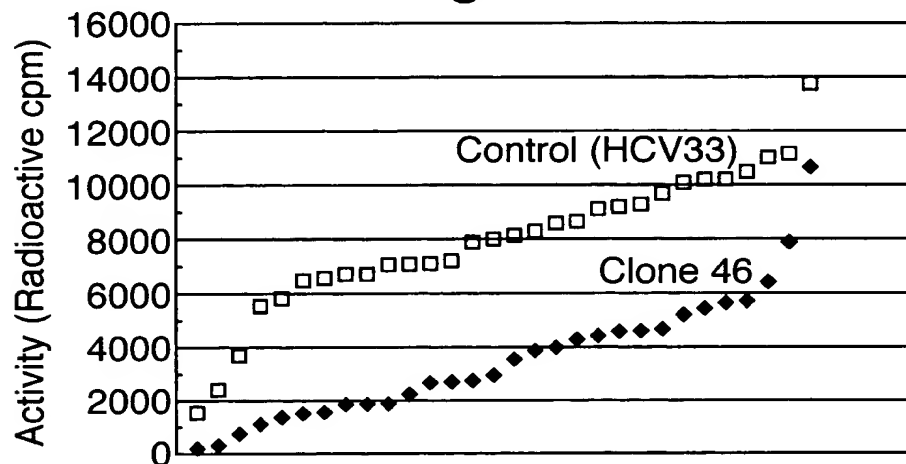


Fig. 15.

NcoI *PstI*

ACCATGGCCCCAGGTGAACTGCAGCAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGGCCCT

T M A Q V K L Q Q S G G G L V Q A G G P

CTGAGGCTCTCCTGTGCAGCCTCTGGACGCACCTTCAGTAACTATGCCGTGGGCTGGTTC

L R L S C A A S G R T F S N Y A V G W F

CGCCAGGCTCCAGGGAAGGAGCGTGAGTTTGTCTGCTGCTATTAGCCGTGATGGTGGGCGC

R Q A P G K E R E F V A A I S R D G G R

ACATACTATGCGGACTCCGTGAAGGGCCGATTTCGCCGTCTCCAGAGACTACGCCGAGAAC

T Y Y A D S V K G R F A V S R D Y A E N

ACGGTGTATCTGCAAATGAACAGCCTGAAACCTGAGGACACGGCCGTTTATTACTGTAAC

T V Y L Q M N S L K P E D T A V Y Y C N

ACAAGGGCCTACTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCAGCGCACCCACAGCGAA

T R A Y W G Q G T Q V T V S S A H H S E

GACCCCAGCTCCGCGGCCCGCCCATCACCATCACCATCACGGGGCCGCAGAACAAAACTC

D P S S A A A H H H H H H G A A E Q K L

ATCTCAGAAGAGGATCTGAATTCTGAGAAAGATGAGCTATGCAATTG

I S E E D L N S E K D E L *MunI*

Fig.16.

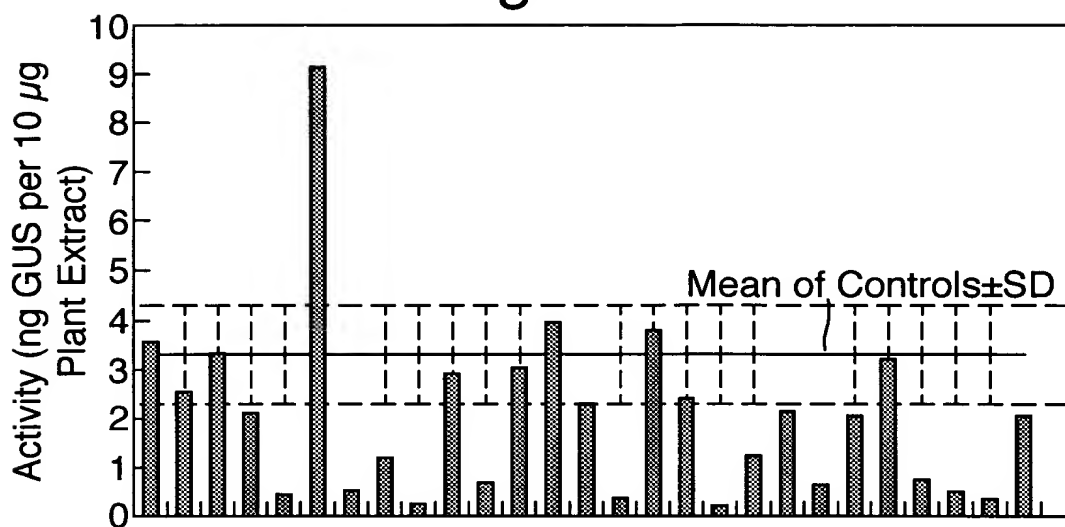


Fig.17A.

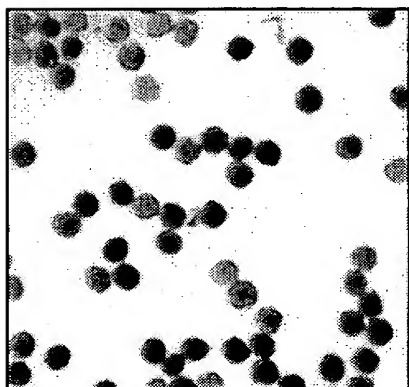
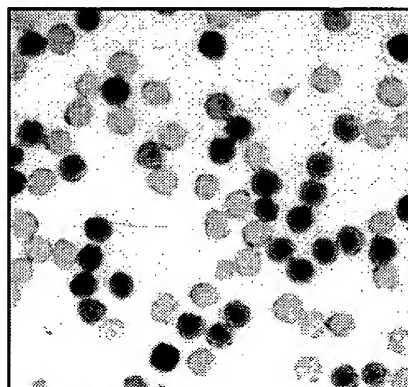


Fig.17B.



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Fig.18.

NcoI PstI

 1 ccattgaggt gcagctgcag gagtcagggg gaggattggt gcaggctggg
 >>.....HCV33.....>
 m e v q l q e s g g g l v q a g

 51 ggctctctga gactctctg tgcagcctcg ggacgcgcca ccagtgggtca
 >.....HCV33.....>
 g s l r l s c a a s g r a t s g

 101 tggtcactat ggtatgggct ggttccgcca ggttccaggg aaggagcgtg
 >.....HCV33.....>
 h g h y g m g w f r q v p g k e r

 151 agtttgtcgc agctattagg tggagtggta aagagacatg gtataaagac
 >.....HCV33.....>
 e f v a a i r w s g k e t w y k d

 201 tccgtgaagg gccgattcac catctccaga gataacgcca agactacggt
 >.....HCV33.....>
 s v k g r f t i s r d n a k t t

 251 ttatctgcaa atgaacagcc tgaaacctga agatacggcc gtttattatt
 >.....HCV33.....>
 v y l q m n s l k p e d t a v y y

 301 gtgccgctcg accgggtcgc gtggatgata tttccctgcc ggttgggttt
 >.....HCV33.....>
 c a a r p v r v d d i s l p v g f
 BstEII

 351 gactactggg gccaggggac ccagggtcacc gtctcctcag aaccaagac
 >.....HCV33.....>>>>..Hinge..
 d y w g q g t q v t v s s e p k

 401 accaaaacca caaccacaac cacaaccaca accacaaccc aatcctacaa
 >.....Hinge.....>
 t p k p q p q p q p q p n p t

 451 cagaatccaa gtgtcccaaa tgtccagccc ctgagctcct gggagggccc
 >.....Hinge.....>>>>.....CH2.....>
 t e s k c p k c p a p e l l g g p

 501 tcagtcttca tcttcccccc gaaaccaag gacgtcctct ccatttctgg
 >.....CH2.....>
 s v f i f p p k p k d v l s i s

 551 gagggccgag gtcacgtgcg ttgtggtaga cgtgggcccag gaagaccccc
 >.....CH2.....>
 g r p e v t c v v v d v g q e d p

 601 aggtcagttt caactggtac attgatggcg cagaggtgcy aacggccaac
 >.....CH2.....>
 e v s f n w y i d g a e v r t a n

 651 acgaggccaa aagaggaaca gttcaacagc acgtaccgcy tggtcagcgt
 >.....CH2.....>

09737476.121800

Fig.18 (Cont).

t r p k e e q f n s t y r v v s

701 cctgcccac cagcaccagg actggctgac ggggaaagag ttcaaagca
 >.....CH2.....>
 v l p i q h q d w l t g k e f k c
 HincII

751 aggtcaacaa caaagctctc ccggccccca tcgagaagac catctccaag
 >.....CH2.....>
 k v n n k a l p a p i e k t i s k

801 gccaaagggc agaccggga gccgcaggtg tacgccctgg cccacacccg
 >...>>>.....CH3.....>
 a k g q t r e p q v y a l a p h

851 ggaagagctg gccaaaggaca ccgtgagcgt aacctgcctg gtcaaaggct
 >.....CH3.....>
 r e e l a k d t v s v t c l v k g

901 tctaccacac tgatatcaac gttgagtggc agaggaacgg tcagccggag
 >.....CH3.....>
 f y p p d i n v e w q r n g q p e

951 tcagagggca cctacgccac cagccaccc cagctggaca acgacgggac
 >.....CH3.....>
 s e g t y a t t p p q l d n d g

1001 ctacttcctc tacagcaagc tctcggtggg aaagaacacg tggcagcggg
 >.....CH3.....>
 t y f l y s k l s v g k n t w q r

1051 gagaaacctt cacctgtgtg gtgatgcacg aggccttgca caaccactac
 >.....CH3.....>
 g e t f t c v v m h e a l h n h y
 EcoRI

1101 acccagaaat ccatcaccca gtcttcgggt aaataataag aattcgagct
 >.....CH3.....>>
 t q k s i t q s s g k

1151 cgaa

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Fig.19.

```

      NcoI          PstI
      -----
1  ccatggaggt gcagctgcag gagtcagggg gaggattggt gcaggctggg
   >>.....HCV33.....>
     m e v q l q e s g g g l v q a g

51  ggctctctga gactctcctg tgcagcctcg ggacgcgcca ccagtgggtca
   >.....HCV33.....>
     g s l r l s c a a s g r a t s g

101  tggtcactat ggtatgggct ggttccgcca ggttccaggg aaggagcgtg
   >.....HCV33.....>
     h g h y g m g w f r q v p g k e r

151  agtttgtcgc agctattagg tggagtggta aagagacatg gtataaagac
   >.....HCV33.....>
     e f v a a i r w s g k e t w y k d

201  tccgtgaagg gccgattcac catctccaga gataacgcca agactacggt
   >.....HCV33.....>
     s v k g r f t i s r d n a k t t

251  ttatctgcaa atgaacagcc tgaaacctga agatacggcc gtttattatt
   >.....HCV33.....>
     v y l q m n s l k p e d t a v y y

301  gtgccgctcg accggtccgc gtggatgata tttccctgcc ggttggggtt
   >.....HCV33.....>
     c a a r p v r v d d i s l p v g f
                          BstEII
                          -----
351  gactactggg gccaggggac ccaggtcacc gtctcctcag aacccaagac
   >.....HCV33.....>>>>..Hinge..>
     d y w g q g t q v t v s s e p k

401  accaaaacca caaccacaac cacaaccaca accacaaccc aatcctacaa
   >.....Hinge.....>
     t p k p q p q p q p q p n p t

451  cagaatccaa gtgtcccaaa tgtccagccc ctgagctcct gggagggccc
   >.....Hinge.....>>>>.....CH2.....>
     t e s k c p k c p a p e l l g g p

501  tcagtcttca tcttcccccc gaaaccaag gacgtcctct ccatttctgg
   >.....CH2.....>
     s v f i f p p k p k d v l s i s

551  gagggccgag gtcacgtgcg ttgtggtaga cgtgggccag gaagaccccg
   >.....CH2.....>
     g r p e v t c v v v d v g q e d p

601  aggtcagttt caactggtac attgatggcg cagaggtgcg aacggccaac
   >.....CH2.....>
     e v s f n w y i d g a e v r t a n

651  acgaggccaa aagaggaaca gttcaacagc acgtaccgcg tggtcagcgt
   >.....CH2.....>

```

093746-121800

Fig.19 (Cont).

t r p k e e q f n s t y r v v s
 701 cctgcccattc cagcaccagg actggctgac ggggaaagag ttcaaagca
 >.....CH2.....>
 v l p i q h q d w l t g k e f k c
 HincII

 751 aggtcaacaa caaagctctc ccggccccc tgcagaagac catctccaag
 >.....CH2.....>
 k v n n k a l p a p i e k t i s k
 801 gccaaagggc agaccggga gccgcaggtg tacgccctgg cccacacccg
 >...>>>.....CH3.....>
 a k g q t r e p q v y a l a p h
 851 ggaagagctg gccaaaggaca ccgtgagcgt aacctgcctg gtcaaaggct
 >.....CH3.....>
 r e e l a k d t v s v t c l v k g
 901 tctaccacc tgatatcaac gttgagtggc agaggaacgg tcagccggag
 >.....CH3.....>
 f y p p d i n v e w q r n g q p e
 951 tcagagggca cctacgccac cagccaccc cagctggaca acgacgggac
 >.....CH3.....>
 s e g t y a t t p p q l d n d g
 1001 ctacttcctc tacagcaagc tctcgggtggg aaagaacacg tggcagcggg
 >.....CH3.....>
 t y f l y s k l s v g k n t w q r
 1051 gagaaacctt cacctgtgtg gtgatgcacg aggccctgca caaccactac
 >.....CH3.....>
 g e t f t c v v m h e a l h n h y
 1101 acccagaaat ccatcaccca gtcttcgggt aaatctgaga aagatgagct
 >.....CH3.....>>>>.....SEKDEL.....>
 t q k s i t q s s g k s e k d e
 EcoRI

 1151 ataataagaa ttcgagctcg aa
 >
 l

Fig.20.

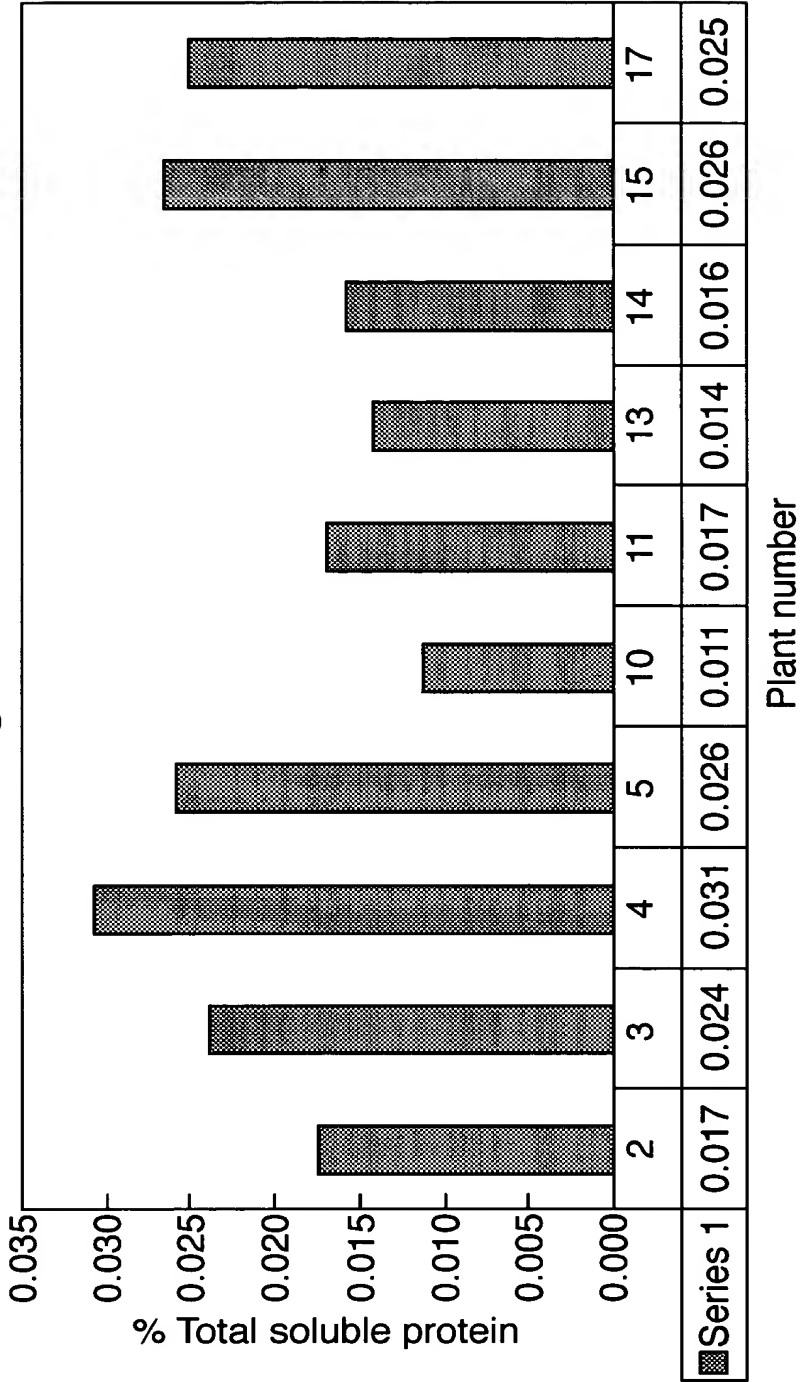


Fig.21.

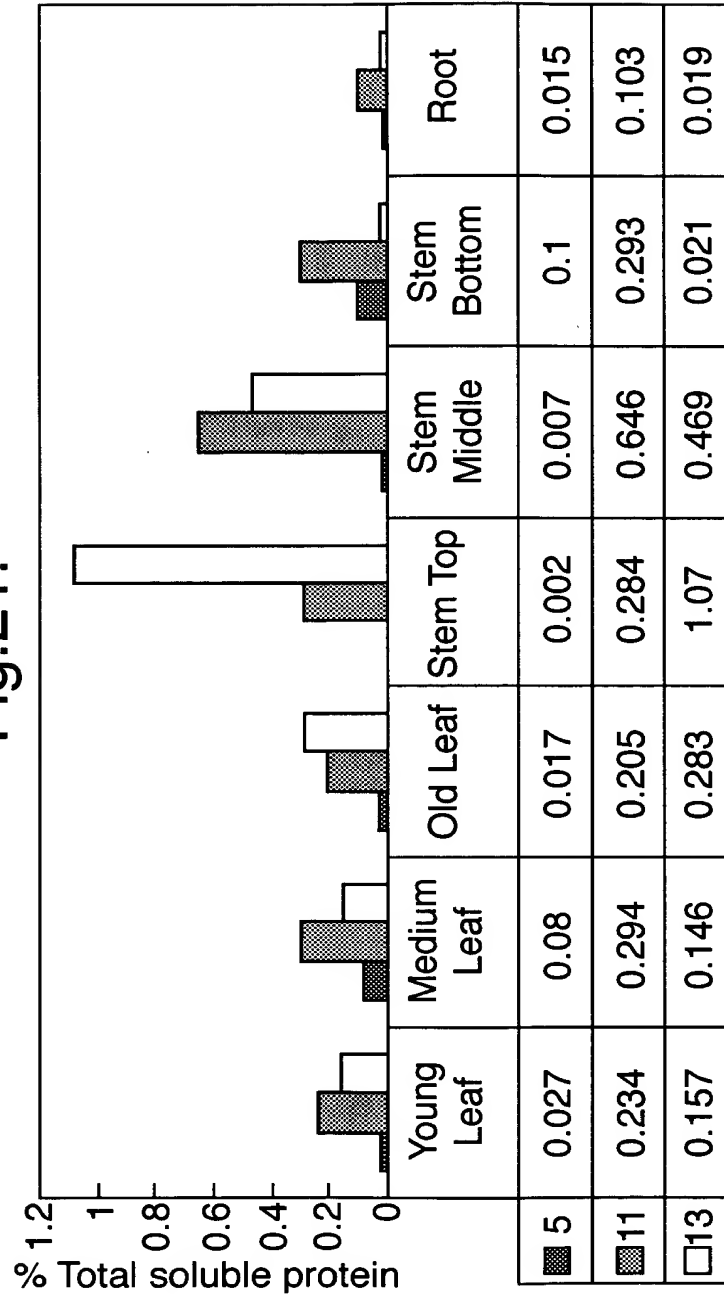


Fig.22.

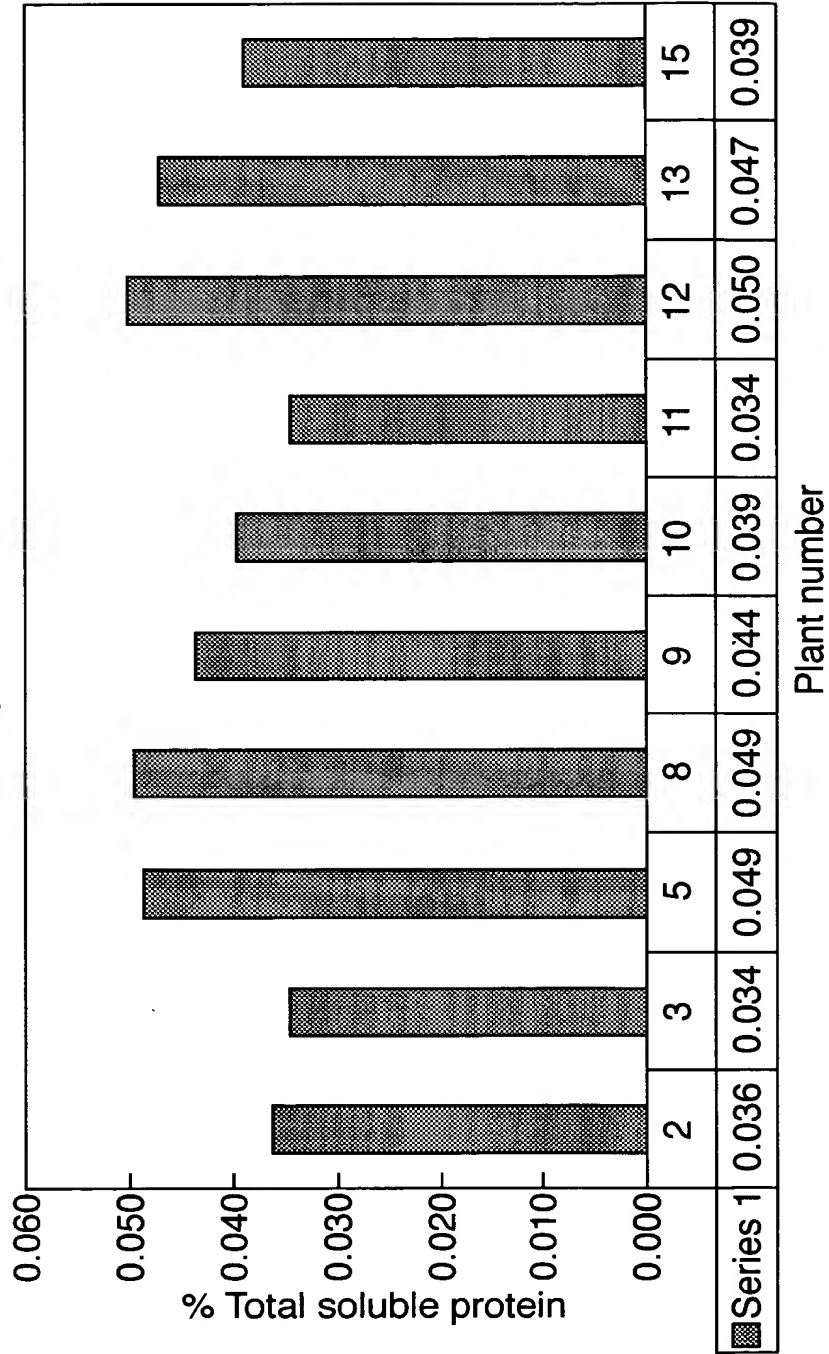


Fig.23.

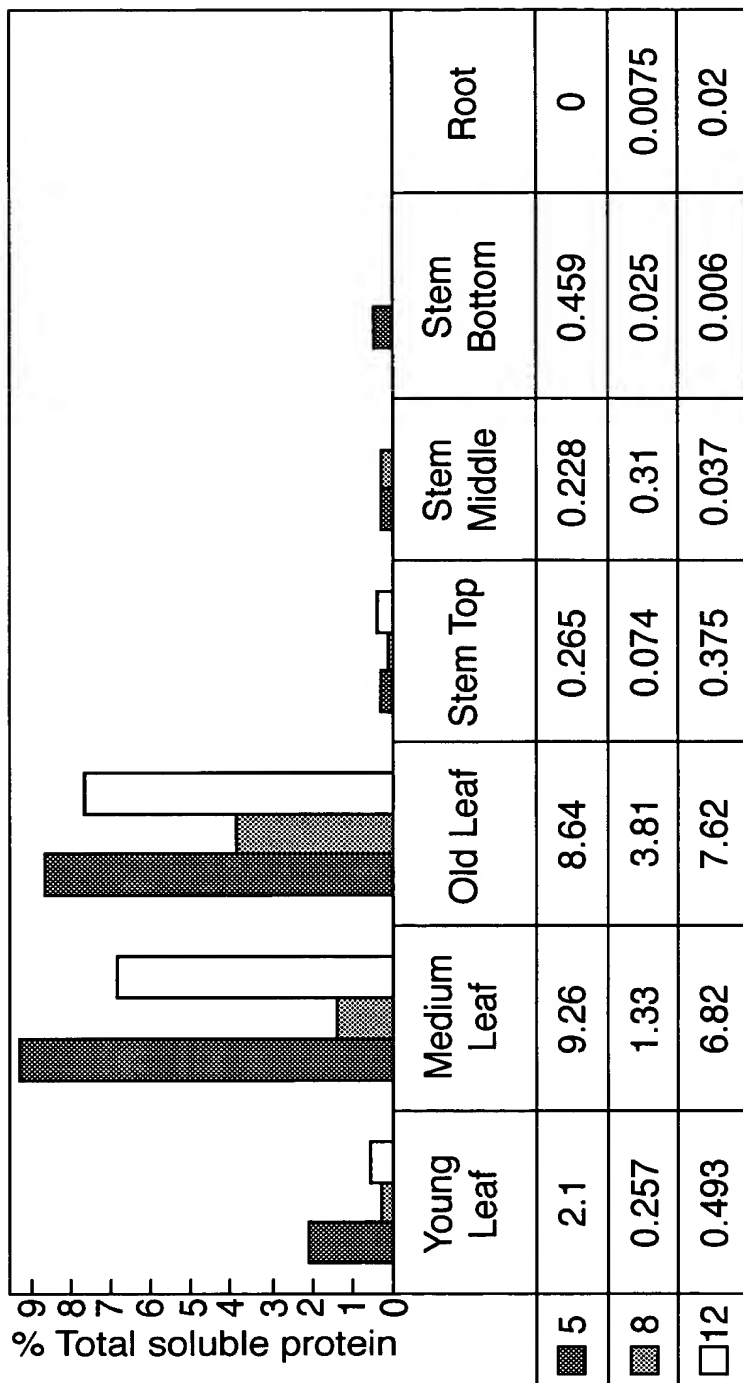


Fig.24.

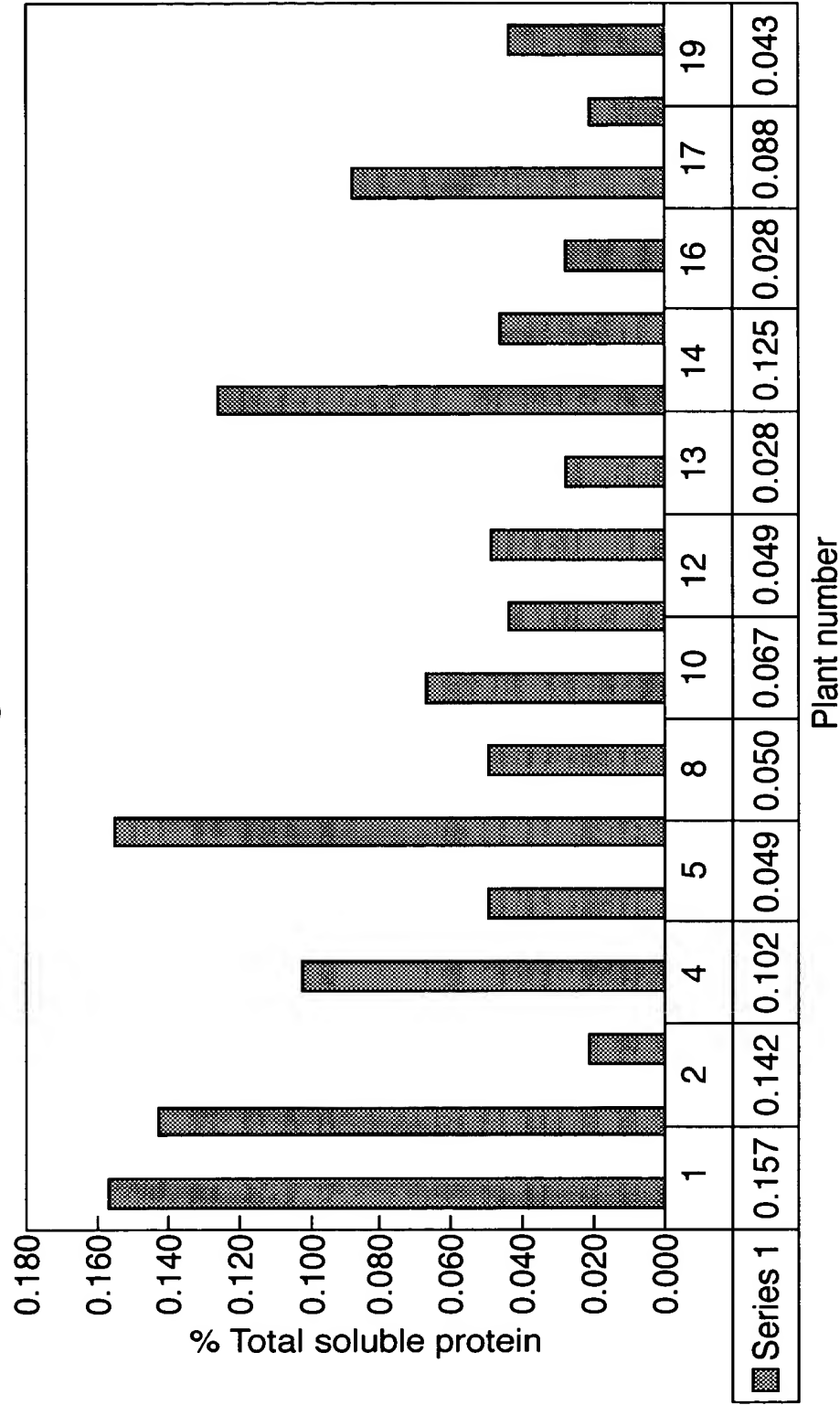


Fig.25.

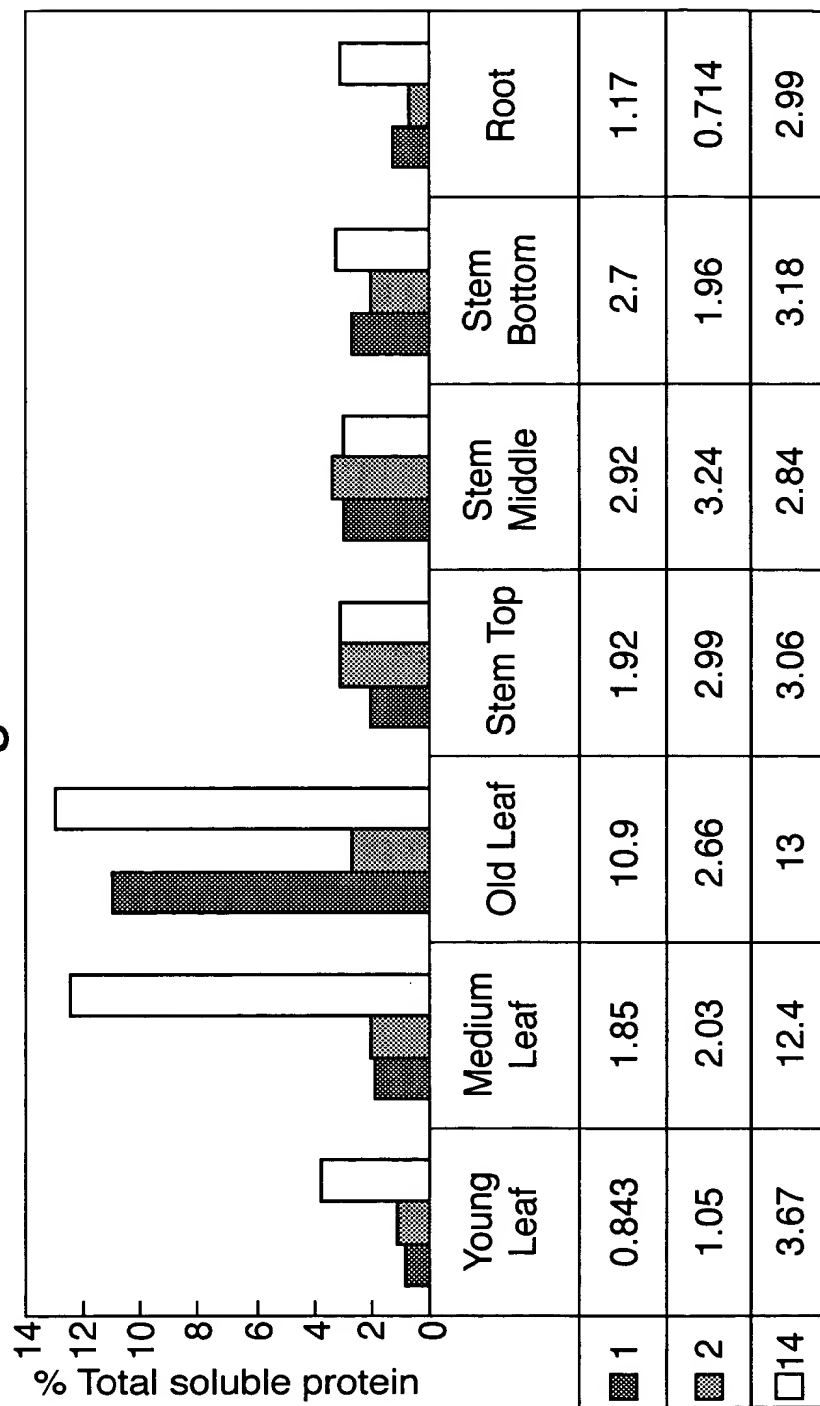


Fig.26.

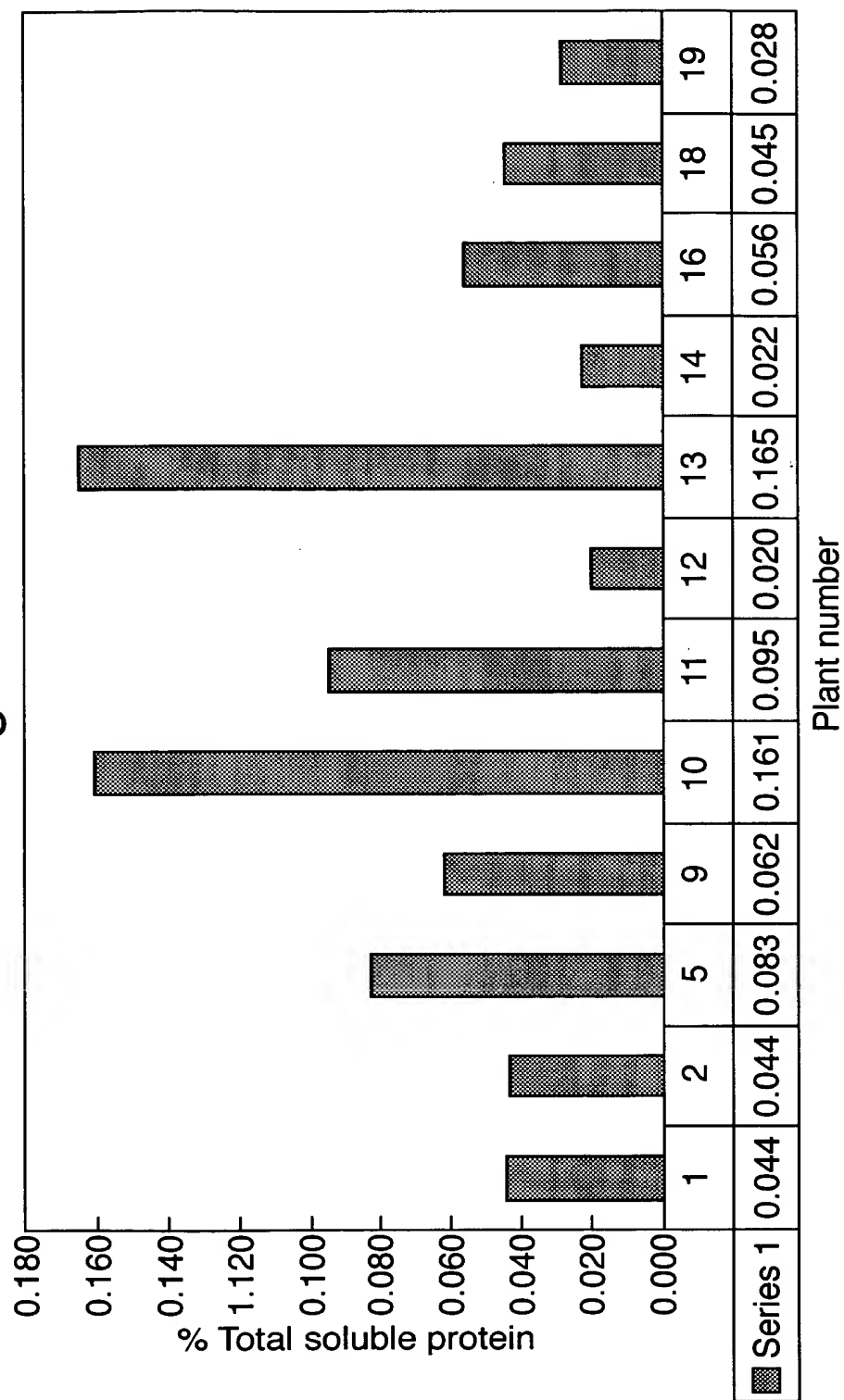


Fig.27.

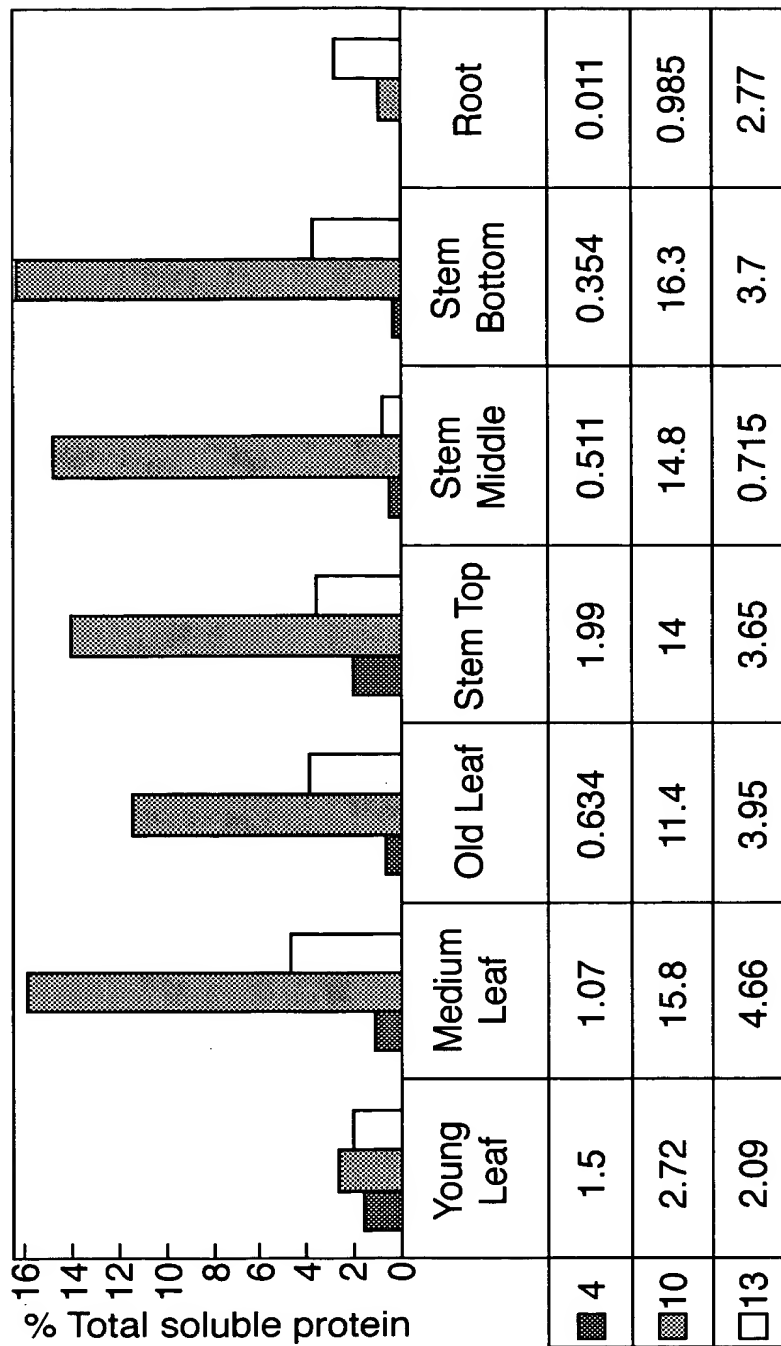


Fig.28.

NcoI PstI

 1 ccattggccca ggtgcagctg caggagtctg ggggaggctt ggtgcaggct
 M A Q V Q L Q E S G G G L V Q A
 51 ggggggtctc tgaggctctc ctgtgcagcc tctggaagca ttttcagacg
 G G S L R L S C A A S G S I F R
 101 tccgcattatg ggttgggttcc gccaggctcc agggcaggag cgcgagttgg
 R P H M G W F R Q A P G Q E R E L
 151 tcgcactgat ttctgcgggt ggtcgtacat ggtatgcaga ctccgtgaag
 V A L I S A G G R T W Y A D S V K
 201 ggccgattca ccattctccag agacaacgcc aagaacacgc tgtatctgca
 G R F T I S R D N A K N T L Y L
 251 aatgaacagc ctgaaacctg aggacacggc cgttttattac tgtactgccg
 Q M N S L K P E D T A V Y Y C T A
 BstEII

 301 ggggttcgta ctggggccag gggacccagg tcaccgtcgc ctcagaaccc
 G G S Y W G Q G T Q V T V A S E P
 351 aagacaccaa aaccacaacc agcggccgcc catcaccatc accatcacgg
 K T P K P Q P A A A H H H H H H
 401 ggccgcagaa caaaaactca tctcagaaga ggatctgaat ggggcccgat
 G A A E Q K L I S E E D L N G A A
 MunI

 451 agtaacaatt g

008721 924260

Fig.29.

